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Gln Val Ile Ser Met Lys Leu Val Thr Pro Ala Lys Gly Thr Ile Glu 245 250 255

Leu Ser Arg Glu Lys Asp Pro Glu Leu Phe His Leu Ala Arg Cys Gly 260 265 270

Leu Gly Gly Leu Gly Val Val Ala Glu Val Thr Leu Gln Cys Val Ala 275 280 285

Arg His Glu Leu Val Glu His Thr Tyr Val Ser Asn Leu Gln Glu Ile 290 295 300

Lys Lys Asn His Lys Lys Leu Leu Ser Ala Asn Lys His Val Lys Tyr 305 310 315 320

Leu Tyr Ile Pro Tyr Thr Asp Thr Val Val Val Val Thr Cys Asn Pro 325 330 335

Val Ser Lys Trp Ser Gly Pro Pro Lys Asp Lys Pro Lys Tyr Thr Thr 340 345 350

Asp Glu Ala Val Gln His Val Arg Asp Leu Tyr Arg Glu Ser Ile Val 355 360 365

Lys Tyr Arg Val Gln Asp Ser Gly Lys Lys Ser Pro Asp Ser Ser Glu 370 375 380

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Asp Glu Ile Leu Gly Phe Asp Cys Gly Gly Gln Gln Trp Val Ser Glu 435 440 445

Ser Cys Phe Pro Ala Gly Thr Leu Ala Asn Pro Ser Met Lys Asp Leu 450 460

Glu Tyr Ile Glu Glu Leu Lys Lys Leu Ile Glu Lys Glu Ala Ile Pro 465 470 475 480

Ala Pro Ala Pro Ile Glu Gln Arg Trp Thr Ala Arg Ser Lys Ser Pro $485 \hspace{1cm} 490 \hspace{1cm} 495 \hspace{1cm}$

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Ala Leu Phe Ser Gly Ala Ala Thr Tyr Phe Ser Phe Pro Phe Pro Glu 65 70 75 80

Asn Ala Lys His Lys Lys Ala Gln Ile Phe Arg Tyr Ala Pro Leu Pro 85 90 95

Glu Asp Leu His Thr Val Ser Asn Trp Ser Gly Thr His Glu Val Gln 100 105 110

Thr Arg Asn Phe Asn Gln Pro Glu Thr Leu Ala Asp Leu Glu Ala Leu 115 120 125

Val Lys Glu Ala His Glu Lys Lys Asn Arg Ile Arg Pro Val Gly Ser 130 135 140

Gly Leu Ser Pro Asn Gly Ile Gly Leu Ser Arg Ser Gly Met Val Asn 145 150 155 160

Leu Ala Leu Met Asp Lys Val Leu Glu Val Asp Lys Glu Lys Lys Arg 165 170 175

Val Arg Val Gln Ala Gly Ile Arg Val Gln Gln Leu Val Asp Ala Ile 180 185 190

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210

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Glu Trp Gly Cys Pro Met Asp Asn Gly Leu Glu Val Leu Arg Ser Leu 325 330 335

Asp His Ser Ile Ala Gln Ala Ala Ile Asn Lys Glu Phe Tyr Val His 340 345 350

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Lys Val Glu Glu Trp Tyr Gly Glu Asp Leu Lys Lys Phe Arg Lys Ile 485 490 495

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1581

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Leu Asp Ala Glu Asn Asp Pro Glu Val Phe Lys Ala Ala Leu Leu Ser 165 170 175

Val Gly Lys Ile Gly Ile Ile Val Ser Ala Thr Ile Arg Val Val Pro 180 185 190

Gly Phe Asn Ile Lys Ser Thr Gln Glu Val Ile Thr Phe Glu Asn Leu 195 200 205

Leu Lys Gln Trp Asp Thr Leu Trp Thr Ser Ser Glu Phe Ile Arg Val 210 215 220

Trp Trp Tyr Pro Tyr Thr Arg Lys Cys Val Leu Trp Arg Gly Asn Lys 225 230 235 240

Thr Thr Asp Ala Gln Asn Gly Pro Ala Lys Ser Trp Trp Gly Thr Lys 245 250 255

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Tyr Gly Lys Leu Glu Lys Ser Ser Thr Gly Asp Val Asn Val Thr Asp 290 295 300

Ser Ile Ser Gly Phe Asn Met Asp Cys Leu Phe Ser Gln Phe Val Asp 305 310 315 320

Glu Trp Gly Cys Pro Met Asp Asn Gly Leu Glu Val Leu Arg Ser Leu 325 330 335

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Leu Asp Thr Ser Lys Arg Thr Asn Thr Ser Pro Gly Pro Val Tyr Gly 370 375 380

Asn Val Cys Arg Pro Phe Leu Asp Asn Thr Pro Ser His Cys Arg Phe 385 390 395 400

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Pro Thr Ile Tyr Arg Pro Phe Gly Cys Asn Thr Pro Ile His Lys Trp 420

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Trp Ala Lys Asn Phe Leu Gly Ser Thr Thr Leu Ala Ala Gly Pro Val 450

Lys Lys Asp Thr Asp Tyr Asp Asp Phe Glu Met Arg Gly Met Ala Leu 465

Lys Val Glu Glu Trp Tyr Gly Glu Asp Leu Lys Lys Phe Arg Lys Ile 485

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His Pro Gln Leu Asp Glu His Gly Leu Ala Met Ser Asn Leu Gly Ala 100 105 110

Val Ser Asp Val Thr Val Ala Gly Val Ile Gly Ser Gly Thr His Asn 115 120 125

Thr Gly Ile Lys His Gly Ile Leu Ala Thr Gln Val Val Ala Leu Thr 130 135 140

Leu Met Thr Ala Asp Gly Glu Val Leu Glu Cys Ser Glu Ser Arg Asn 145 150 155 160

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Ser Asn Leu Ser His Lys Ile Phe Thr Tyr Glu Cys Arg Phe Lys Gln 290 295 300

His Val Gln Asp Trp Ala Ile Pro Arg Glu Lys Thr Lys Glu Ala Leu 305 310 315 320

Leu Glu Leu Lys Ala Met Leu Glu Ala His Pro Lys Val Val Ala His 325 330 335

Tyr Pro Val Glu Val Arg Phe Thr Arg Gly Asp Asp Ile Leu Leu Ser 340 345 350

Pro Cys Phe Gln Arg Asp Ser Cys Tyr Met Asn Ile Ile Met Tyr Arg 355 360 365

Pro Tyr Gly Lys Asp Val Pro Arg Leu Asp Tyr Trp Leu Ala Tyr Glu 370 375 380

Thr Ile Met Lys Lys Phe Gly Gly Arg Pro His Trp Ala Lys Ala His 385 390 395 400

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Phe Cys Asp Ile Arg Glu Lys Leu Asp Pro Thr Gly Met Phe Leu Asn $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430 \hspace{1.5cm}$

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Primer for L-galactono-1,4-lactone dehydrogenase from A. thaliana

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cerevisiae

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170

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